



SEQUENCE LISTING

<110> Short, Jay M.
Kretz, Keith A.
Gray, Kevin A.
Barton, Nelson Robert
Garrett, James B.
O' Donoghue, Eileen
Mathar, Eric J.

<120> RECOMBINANT BACTERIAL PHYTASES AND USES
THEREOF

<130> 19011-129036

<140> US 1996-06-379

<141> 2001-05-24

<150> US 99-080,515

<151> 2000-04-25

<160> US 99-048,528

<161> 1999-06-25

<170> US 99-191,931

<171> 1999-04-13

<180> US 99-159,214

<181> 1999-04-11

<190> US 98-010,798

<191> 1997-04-13

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<213> DNA

<214> Escherichia coli

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<221> CDS

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<230> misc_feature

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48

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1

5

10

15

cag caa tct gca ttc gct cag agt gag cag gag atg aag atg gaa agt

96

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NOV 22 2002

TECH CENTER 1600/2900

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Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	
		35					40					45				
caa	ctg	atg	cag	gat	gtc	acc	cca	gac	gca	tgg	cca	acc	tgg	ccg	gta	182
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	
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Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	
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aag	ggc	tgc	ccg	cag	tct	ggg	cag	gtc	ggg	att	att	ggt	gat	gtc	gac	336
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	
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Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	
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gac	tgt	gca	ata	acc	gta	cat	acc	cag	gca	gat	acg	tcc	agt	ccc	gat	432
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	
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ccg	tta	tta	aat	cct	cta	aaa	act	ggc	gtt	tgc	caa	ctg	gat	aac	ggg	480
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Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	
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Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	
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Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	
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gag	ata	tta	ctc	ctg	caa	caa	gca	cag	gga	atg	ccg	gag	ccg	ggg	tgg	768
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	

21
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aac ggg caa ttt tat ttg cta caa cgc acg coa gag gtt ggc cgc agc Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser 275	280	235	864
ggc ggc acc ccg tta ttg gat ttg atc atg gca ggc ttg acg ccc cat Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His 290	295	300	912
cca ccg caa aaa cag ggc tat ggt gtg aca tta ccc act tca gta ctg Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu 305	310	315	960
ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu 325	330	335	1008
gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly 340	345	350	1056
ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln 355	360	365	1104
tgg att cag gtt tgg ctg gtc ttc cag act tta cag cag atg cgt gat Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp 370	375	380	1152
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr 385	390	395	1200
ctg gca gga tgt gaa gag cga aat ggc cag ggc atg tgt tag ttg gca Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala 405	410	415	1248
ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg ggc tgc agt ttg Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu 420	425	430	1296
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<213>: Escherichia coli

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 Ser Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
 50 55 60
 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
 65 70 75 80
 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
 85 90 95
 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
 100 105 110
 Gln Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
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 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
 130 135 140
 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
 145 150 155 160
 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
 165 170 175
 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
 180 185 190
 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
 195 200 205
 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
 210 215 220
 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
 225 230 235 240
 Thr Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
 245 250 255
 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 260 265 270
 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 280 285
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
 290 295 300
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 390 395 400
 Leu Ala Gly Cys Gln Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
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 Arg Ser His His His His His His
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R!
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 tpatgagggg cattagcacc gcattcaggca atcaataatg tcagatatga aaagcggaaa 181
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1110 - 6

1111 - 1901

1112 - DNA

1113 - Escherichia coli

1200 -

1201 - misc_feature

1202 - 403

1203 - n = A,T,C or G

1400 - 6

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1110 - 7

1111 - 1901

1112 - DNA

1113 - Escherichia coli

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catatcg atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg	240
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro	
1 5 10	
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Leu Thr Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu	
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gaa agt gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag	360
Glu Ser Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys	
35 40 45	
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Pro Val Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala	
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Tyr Leu Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu	
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Ala Lys Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp	
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Val Asp Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu	
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Ala Pro Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser	
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ccc gat ccg tta ttt aat cct cta aaa act gcc gtt tgc caa ctg gat	780
Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp	
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aac gcc aac gtg act gac gcc atc ctg agc agg gca gga ggg tca att	840
Asn Ala Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile	
160 165 170	

B1
C11

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Val Leu Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln	
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Leu Thr Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro	
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Gly Trp Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser	
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Pro His Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser	
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Val Leu Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly	
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Ala Leu Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro	
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Pro Gly Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn	
355 360 365	
agg cag tgg att cag gtt tgc ctg gtc ttc cag act tta cag cag atg	1333
Ser Gln Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met	
370 375 380	
cgt gat aaa acc ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa	1381
Arg Asp Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys	
385 390 395	
ctg acc ctg gca gga tgt gaa gag cga aat ggg cag ggc atg tgt tgc	1429

B1
Cont

Leu Thr Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser
400 405 410

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Leu Ala Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys
415 420 425 430

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Ser Leu

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210 8

211 432

212 PFT

213 Escherichia coli

400 8

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
1 5 10 15
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
20 25 30
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
35 40 45
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
50 55 60
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
65 70 75 80
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
85 90 95
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
100 105 110
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
115 120 125
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
130 135 140
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
145 150 155 160
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
165 170 175
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
180 185 190
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
195 200 205
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
210 215 220
Arg Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
225 230 235 240
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
245 250 255

B1
Cont

Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 260 265 270
 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 280 285
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His
 290 295 300
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 390 395 400
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
 405 410 415
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
 420 425 430

-110- 9

-111- 1308

-112- DNA

-113- Artificial Sequence

-116-

-113- modified phytase enzyme

-121- CDS

-122- (1)...(1308)

-170- 9

atg aag gag atc tta atc cca ttt tta tct ctt ctg att ccg tta acc 48
 Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
 1 3 10 15
 ccg caa tct gaa ttc gct cag agt gag ccg gag ctg aag ctg gaa agt 96
 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
 20 25 30
 atg ctg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg 144
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
 35 40 45
 aag ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta 192
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
 50 55 60
 aag ctg ggt gag ctg aca ccg ccg ggt ggt gag cta atc gcc tat ctc 240
 Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
 65 70 75 80
 gga cat cac tgg cgt cag ccg ctg gla gcc gac gga ttg ctg cct aaa 288
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys

B
 Cat

85	90	95
tgt ggc tgc cag cag tgc ggc cag tgc ggc att att gat gat ggc gat Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp 100 105 110	336	
gag cgt acc cgt aaa aca ggc gaa ggc ttc ggc ggc ggg ctg gca cct Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro 115 120 125	384	
gac tgt gca ata acc gta cat acc cag gca gat acg tac agt ccc gat Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp 130 135 140	432	
cag tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac ggc Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala 145 150 155 160	480	
aac gtg act gac ggc atc ctc gag agg gca gga ggg tca att gct gac Asn Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp 165 170 175	528	
ttt acc ggg cat tat caa acg ggc ttt cgc gaa ctg gaa cgg gtg ctt Phe Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu 180 185 190	576	
aat ttt cag caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu 195 200 205	624	
agc tgt tca tta acg cag gca tta cca tgc gaa ctc aag gtg agc ggc Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala 210 215 220	672	
gac tgt gtc tca tta acc ggt ggc gta agc ctc gca tca atg ctg acc Asp Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr 225 230 235 240	720	
gag ata ttt ctc ctg caa caa gca cag gga atg ccc gag ccc ggg tgg Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp 245 250 255	768	
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His 260 265 270	816	
aac ggc caa ttt gat ttg cta caa cgc acg cca gag gtt ggc cgc agc Asn Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser 275 280 285	864	
cgc gcc acc ccg tta tta gat ttg atc aag aca ggc ttg acg ccc cat Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His 290 295 300	912	
cca ccg caa aaa cag ggc tat ggt gtg aca tta ccc act tca gtg ctg Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu 305 310 315 320	960	

ttt atc ggc gga gag gat ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt	1108
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu	
321 340 335	
gaq ctc aac tgg acg ctt ccc ggt cag cag gat aac acg cag cca ggt	1056
Gln Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
340 345 350	
ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag	1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
355 360 365	
tgg att cag gtt tgg ctg gtc ttc cag act tta cag cag atg cgt gat	1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
370 375 380	
aaa acg ccg ctg tca tta aat acg cag ccc gga gag gtg aaa ctg acc	1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
385 390 395 400	
atc tca gga tgt gaa gag cga aat ggc cag ggc atg tgt tgg ttg gca	1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala	
405 410 415	
ggt ttt acg caa atc gtg aat gaa gca cgc ata cag ggc tgc agt ttg	1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu	
420 425 430	
aaa tct cat cta	1308
Arg Ser His Leu	
435	

4210 - 10
 4211 - 436
 4212 - PRT
 4213 - Artificial Sequence

4214 -
 4215 - modified phytase enzyme

4400 - 10
 Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
 1 5 10 15
 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
 20 25 30
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
 35 40 45
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
 50 55 60
 Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
 65 70 75 80
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys
 85 90 95
 Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
 100 105 110

Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
 115 125 125
 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
 131 135 145
 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
 141 150 155 160
 Asn Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp
 161 170 175
 Phe Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
 180 185 190
 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
 195 200 205
 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
 210 215 220
 Asp Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
 221 230 235 240
 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
 245 250 255
 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 260 265 270
 Asn Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 280 285
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His
 290 295 300
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 390 395 400
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
 405 410 415
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
 420 425 430
 Arg Ser His Leu
 435